10. Improvement of cotton fiber quality through Marker-Assisted Breeding: limits and prospects of a QTL approach

***LACAPE JEAN-MARC**, CIRAD, Avenue Agropolis, Montpellier cedex 5, France*

The marker-assisted introgression of quantitative traits in crop plants is the topic of an ever-increasing number of reports (recent interrogation of bibliographic database using marker-assisted breeding or QTL as key words produced nearly 500 and 2500 hits respectively). Different papers based both on theoretical and experimental evidence, have also emphasized the limits of QTL-based breeding strategies when applied to quantitative traits. Among these limitations the molecular breeder may face are the precision, power and confidence associated to QTL detection, the important number of progenies to be manipulated when the number of QTL increases. A combination of marker-based and classical phenotype-based selections is often recommended. Our program of interspecific *G. hirsutum* / *G. barbadense* marker-assisted backcross selection, MABS, aims at transferring cotton fibre quality QTLs of *G. barbadense* into *G. hirsutum*. In the preceding seasons, the BC1, BC2 and BC2S1 served for 3 separate QTL analyses (Lacape *et al*., Crop Sc, in press). The pooled QTL data from the 3 populations revealed a total of 50 QTLs meeting permutation-based LOD thresholds (between LOD 3.2 and LOD 4.0 on a per-trait basis) for 11 fibre quality-related traits. When reducing the detection threshold to LOD 2.5, this total reached 80 QTLs. Individual phenotypic effects were essentially in the range of 5-15%, and rarely exceeded 20%. The direction of the effect of 70% of the QTLs was as expected from the parental value (better fibre length, strength and fineness conferred by the *G. barbadense* parent, and better maturity and colour conferred by the *G. hirsutum* parent alleles). A majority of the QTLs were co-localized within QTL-rich chromosome regions: when considering only the donor segments, for which positive contributions to fibre quality derived from the presence of the *G. barbadense* alleles, 19 regions on 15 different chromosomes were defined. Interestingly, 1/3rd (26 out of 80) of the QTLs (LOD 2.5) detected confirmed QTLs reported in other interspecific populations. Using these 15 regions as target candidate regions for introgression, we undertook marker-based selection within 411 and 450 plants in each BC_3 and BC_4 generations respectively: ca 10% of individuals were kept at seedling stage based on the presence of *G. barbadense* alleles at chosen SSR and AFLP loci. The allelic constitution of 37 selected BC_3 plants showed that 5 to 16% (8% on average) of donor *G. barbadense* alleles were still present genome-wide, corresponding only to 3 to 6 of the 15 initial QTL-rich target regions. The marker-trait associations in this BC_4 generation only partly confirmed the associations observed in the previous generations (around cases). Some of the BC_4 plants having

introgressed these particular regions however proved highly interesting as regards to their fibre quality. The field evaluation of these BC_4 as F_2 progenies value using agronomical as well as fibre quality measurements was underway during summer 2004.

International Cotton Genome Initiative
ICGI–2004 Workshop

Book of Abstracts

October 10-13, 2004

Hyderabad, Andhra Pradesh, India

International Cotton Genome Initiative

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Issued By:
Dr. P. V. Varadarajan
Secretary, Indian Society
For Cotton Improvement

Compiled And Printed By:
Mr. P. Vidyasagar
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